

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/553,160  
Source: IFW0  
Date Processed by STIC: 05/09/2006

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 05/09/2006

PATENT APPLICATION: US/10/553,160

TIME: 09:42:16

Input Set : A:\A-71973.ST25.txt

Output Set: N:\CRF4\05092006\J553160.raw

3 <110> APPLICANT: Mount Sinai School of Medicine of New York University  
 4 Horvath, Curt  
 5 Rodriguez, Jason  
 6 Ulane, Christina Marie  
 7 Parisien, Jean-Patrick  
 9 <120> TITLE OF INVENTION: Methods and Compositions for Inhibiting STAT Signaling

## Pathways

11 <130> FILE REFERENCE: 28610/US/2 (461089-00071)  
 13 <140> CURRENT APPLICATION NUMBER: US 10/553,160  
 14 <141> CURRENT FILING DATE: 2005-10-14  
 16 <150> PRIOR APPLICATION NUMBER: PCT/US04/12066  
 17 <151> PRIOR FILING DATE: 2004-04-19  
 19 <150> PRIOR APPLICATION NUMBER: US 60/463,764  
 20 <151> PRIOR FILING DATE: 2003-04-17  
 22 <160> NUMBER OF SEQ ID NOS: 13  
 24 <170> SOFTWARE: PatentIn version 3.3  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 224  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Mumps virus  
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 37 Gly Met Asn Val Ala Asn His Phe Leu Ser Ala Pro Ile Gln Gly Thr  
 38 20 25 30  
 41 Asn Ser Leu Ser Lys Ala Ser Ile Ile Pro Gly Val Ala Pro Val Leu  
 42 35 40 45  
 45 Ile Gly Asn Pro Glu Gln Lys Asn Ile Gln His Pro Thr Ala Ser His  
 46 50 55 60  
 49 Gln Gly Ser Lys Ser Lys Gly Ser Gly Ser Gly Val Arg Ser Ile Ile  
 50 65 70 75 80  
 53 Val Pro Pro Ser Glu Ala Gly Asn Gly Gly Thr Gln Ile Pro Glu Pro  
 54 85 90 95  
 57 Leu Phe Ala Gln Thr Gly Gln Gly Gly Ile Val Thr Thr Val Tyr Gln  
 58 100 105 110  
 61 Asp Pro Thr Ile Gln Pro Thr Gly Ser Tyr Arg Ser Val Glu Leu Ala  
 62 115 120 125  
 65 Lys Ile Gly Lys Glu Arg Met Ile Asn Arg Phe Val Glu Lys Pro Arg  
 66 130 135 140  
 69 Thr Ser Thr Pro Val Thr Glu Phe Lys Arg Gly Ala Gly Ser Gly Cys  
 70 145 150 155 160  
 73 Ser Arg Pro Asp Asn Pro Arg Gly Gly His Arg Arg Glu Trp Ser Leu  
 74 165 170 175  
 77 Ser Trp Val Gln Gly Glu Val Arg Val Phe Glu Trp Cys Asn Pro Ile

Cpg-6)

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78          180          185          190
81 Cys Ser Pro Ile Thr Ala Ala Ala Arg Phe His Ser Cys Lys Cys Gly
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90 <211> LENGTH: 675
91 <212> TYPE: DNA
92 <213> ORGANISM: Mumps virus
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97 gcaaatcatt tcctatccgc cccattccag ggaaccaact cgctgagcaa ggcctcaatc      120
99 atccctggcg ttgcacctgt actcattggc aatccagagc aaaagaacat tcagcaccct      180
101 accgcatcac atcagggatc caagtcaaag ggcagcgggt caggggtcag gtccatcata      240
103 gtcccaccct ccgaagcagg caatggaggg actcagattc ctgagcccct ttttgacaaa      300
105 acaggacagg gtggtatagt caccacagtt tatcaggatc caactatcca accaacaggt      360
107 tcataccgaa gtgtggaatt ggcgaagatc ggaaaagaga gaatgattaa tcgatttggt      420
109 gagaaaccta gaacctcaac gccggtgaca gaatttaaga ggggggcccgg gagcggctgc      480
111 tcaaggccag acaatccaag aggagggcat agacgggaat ggagcctcag ctgggtccaa      540
113 ggagaggtcc gggctcttga gtggtgcaac cctatatgct cacctatcac tgccgcagca      600
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121 <211> LENGTH: 770
122 <212> TYPE: PRT
123 <213> ORGANISM: Homo sapiens
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132          20          25          30
135 Phe Leu Ala Pro Trp Ile Glu Ser Gln Asp Trp Ala Tyr Ala Ala Ser
136          35          40          45
139 Lys Glu Ser His Ala Thr Leu Val Phe His Asn Leu Leu Gly Glu Ile
140          50          55          60
143 Asp Gln Gln Tyr Ser Arg Phe Leu Gln Glu Ser Asn Val Leu Tyr Gln
144 65          70          75          80
147 His Asn Leu Arg Arg Ile Lys Gln Phe Leu Gln Ser Arg Tyr Leu Glu
148          85          90          95
151 Lys Pro Met Glu Ile Ala Arg Ile Val Ala Arg Cys Leu Trp Glu Glu
152          100          105          110
155 Ser Arg Leu Leu Gln Thr Ala Ala Thr Ala Ala Gln Gln Gly Gly Gln
156          115          120          125
159 Ala Asn His Pro Thr Ala Ala Val Val Thr Glu Lys Gln Gln Met Leu
160          130          135          140
163 Glu Gln His Leu Gln Asp Val Arg Lys Arg Val Gln Asp Leu Glu Gln
164 145          150          155          160
167 Lys Met Lys Val Val Glu Asn Leu Gln Asp Asp Phe Asp Phe Asn Tyr
168          165          170          175

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172      180      185      190
175 Gln Ser Val Thr Arg Gln Lys Met Gln Gln Leu Glu Gln Met Leu Thr
176      195      200      205
179 Ala Leu Asp Gln Met Arg Arg Ser Ile Val Ser Glu Leu Ala Gly Leu
180      210      215      220
183 Leu Ser Ala Met Glu Tyr Val Gln Lys Thr Leu Thr Asp Glu Glu Leu
184 225      230      235      240
187 Ala Asp Trp Lys Arg Arg Gln Gln Ile Ala Cys Ile Gly Gly Pro Pro
188      245      250      255
191 Asn Ile Cys Leu Asp Arg Leu Glu Asn Trp Ile Thr Ser Leu Ala Glu
192      260      265      270
195 Ser Gln Leu Gln Thr Arg Gln Gln Ile Lys Lys Leu Glu Glu Leu Gln
196      275      280      285
199 Gln Lys Val Ser Tyr Lys Gly Asp Pro Ile Val Gln His Arg Pro Met
200      290      295      300
203 Leu Glu Glu Arg Ile Val Glu Leu Phe Arg Asn Leu Met Lys Ser Ala
204 305      310      315      320
207 Phe Val Val Glu Arg Gln Pro Cys Met Pro Met His Pro Asp Arg Pro
208      325      330      335
211 Leu Val Ile Lys Thr Gly Val Gln Phe Thr Thr Lys Val Arg Leu Leu
212      340      345      350
215 Val Lys Phe Pro Glu Leu Asn Tyr Gln Leu Lys Ile Lys Val Cys Ile
216      355      360      365
219 Asp Lys Asp Ser Gly Asp Val Ala Ala Leu Arg Gly Ser Arg Lys Phe
220      370      375      380
223 Asn Ile Leu Gly Thr Asn Thr Lys Val Met Asn Met Glu Glu Ser Asn
224 385      390      395      400
227 Asn Gly Ser Leu Ser Ala Glu Phe Lys His Leu Thr Leu Arg Glu Gln
228      405      410      415
231 Arg Cys Gly Asn Gly Gly Arg Ala Asn Cys Asp Ala Ser Leu Ile Val
232      420      425      430
235 Thr Glu Glu Leu His Leu Ile Thr Phe Glu Thr Glu Val Tyr His Gln
236      435      440      445
239 Gly Leu Lys Ile Asp Leu Glu Thr His Ser Leu Pro Val Val Val Ile
240      450      455      460
243 Ser Asn Ile Cys Gln Met Pro Asn Ala Trp Ala Ser Ile Leu Trp Tyr
244 465      470      475      480
247 Asn Met Leu Thr Asn Asn Pro Lys Asn Val Asn Phe Phe Thr Lys Pro
248      485      490      495
251 Pro Ile Gly Thr Trp Asp Gln Val Ala Glu Val Leu Ser Trp Gln Phe
252      500      505      510
255 Ser Ser Thr Thr Lys Arg Gly Leu Ser Ile Glu Gln Leu Thr Thr Leu
256      515      520      525
259 Ala Glu Lys Leu Leu Gly Pro Gly Val Asn Tyr Ser Gly Cys Gln Ile
260      530      535      540
263 Thr Trp Ala Lys Phe Cys Lys Glu Asn Met Ala Gly Lys Gly Phe Ser
264 545      550      555      560
267 Phe Trp Val Trp Leu Asp Asn Ile Ile Asp Leu Val Lys Lys Tyr Ile

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268		565		570		575	
271	Leu Ala Leu Trp Asn Glu Gly Tyr Ile Met Gly Phe Ile Ser Lys Glu						
272		580		585		590	
275	Arg Glu Arg Ala Ile Leu Ser Thr Lys Pro Pro Gly Thr Phe Leu Leu						
276		595		600		605	
279	Arg Phe Ser Glu Ser Ser Lys Glu Gly Gly Val Thr Phe Thr Trp Val						
280		610		615		620	
283	Glu Lys Asp Ile Ser Gly Lys Thr Gln Ile Gln Ser Val Glu Pro Tyr						
284	625		630		635		640
287	Thr Lys Gln Gln Leu Asn Asn Met Ser Phe Ala Glu Ile Ile Met Gly						
288		645		650		655	
291	Tyr Lys Ile Met Asp Ala Thr Asn Ile Leu Val Ser Pro Leu Val Tyr						
292		660		665		670	
295	Leu Tyr Pro Asp Ile Pro Lys Glu Glu Ala Phe Gly Lys Tyr Cys Arg						
296		675		680		685	
299	Pro Glu Ser Gln Glu His Pro Glu Ala Asp Pro Gly Ser Ala Ala Pro						
300		690		695		700	
303	Tyr Leu Lys Thr Lys Phe Ile Cys Val Thr Pro Thr Thr Cys Ser Asn						
304	705		710		715		720
307	Thr Ile Asp Leu Pro Met Ser Pro Arg Thr Leu Asp Ser Leu Met Gln						
308		725		730		735	
311	Phe Gly Asn Asn Gly Glu Gly Ala Glu Pro Ser Ala Gly Gly Gln Phe						
312		740		745		750	
315	Glu Ser Leu Thr Phe Asp Met Glu Leu Thr Ser Glu Cys Ala Thr Ser						
316		755		760		765	
319	Pro Met						
320	770						
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326	<213> ORGANISM: Homo sapiens						
328	<400> SEQUENCE: 4						
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331	ccgaggggaac aagccccaac cggatccttg acaggcaccc cggcttggcg ctgtctctcc					120	
333	ccctcggctc ggagaggccc ttcggcctga gggagcctcg ccgcccgtcc ccggcacacg					180	
335	cgcagccccg gcctctcggc ctctgccgga gaaacagttg ggacccctga ttttagcagg					240	
337	atggcccaat ggaatcagct acagcagctt gacacacggt acctggagca gctccatcag					300	
339	ctctacagtg acagcttccc aatggagctg cggcagtttc tggccccttg gattgagagt					360	
341	caagattggg catatgcggc cagcaaagaa tcacatgcca ctttggtggt tcataatctc					420	
343	ctgggagaga ttgaccagca gtatagccgc ttctgcaag agtcgaatgt tctctatcag					480	
345	cacaatctac gaagaatcaa gcagtttctt cagagcaggt atcttgagaa gccaatggag					540	
347	attgcccgga ttgtggcccc gtgcctgttg gaagaatcac gccttctaca gactgcagcc					600	
349	actgcggccc agcaaggggg ccaggccaac caccacacag cagccgtggt gacggagaag					660	
351	cagcagatgc tggagcagca ccttcaggat gtccggaaga gagtgcagga tctagaacag					720	
353	aaaatgaaag tggtagagaa tctccaggat gactttgatt tcaactataa aaccctcaag					780	
355	agtcaaggag acatgcaaga tctgaatgga aacaaccagt cagtgaccag gcagaagatg					840	
357	cagcagctgg aacagatgct cactgcgctg gaccagatgc ggagaagcat cgtgagttag					900	
359	ctggcggggc ttttgtcagc gatggagtac gtgcagaaaa ctctcacgga cgaggagctg					960	
361	gctgactgga agaggcggca acagattgcc tgcattggag gcccgcctca catctgccta					1020	

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365 attaagaaac tggaggagtt gcagcaaaaa gtttcctaca aaggggaccc cattgtacag 1140
367 caccggccga tgctggagga gagaatcgtg gagctgttta gaaacttaat gaaaagtgcc 1200
369 tttgtggtgg agcggcagcc ctgcatgccc atgcatcctg accggccccct cgtcatcaag 1260
371 accggcgctcc agttcactac taaagtcagg ttgctggtca aattccctga gttgaattat 1320
373 cagcttaaaa ttaagtggtg cattgacaaa gactctgggg acgttgagc tctcagagga 1380
375 tcccggaaat ttaacattct gggcacaaa acaaaagtga tgaacatgga agaatccaac 1440
377 aacggcagcc tctctgcaga attcaaacac ttgacctga gggagcagag atgtgggaat 1500
379 gggggccgag ccaattgtga tgcttccttg attgtgactg aggagctgca cctgatcacc 1560
381 tttgagaccg aggtgtatca ccaaggcctc aagattgacc tagagacca ctccttgcca 1620
383 gttgtggtga tctccaacat ctgtcagatg ccaaatgcct gggcgctccat cctgtggtac 1680
385 aacatgctga ccaacaatcc caagaatgta aactttttta ccaagcccccc aattggaaacc 1740
387 tgggatcaag tggccgaggt cctgagctgg cagttctcct ccaccaccaa gcgaggactg 1800
389 agcatcgagc agctgactac actggcagag aaactcttgg gacctggtgt gaattattca 1860
391 ggggtgtcaga tcacatgggc taaattttgc aaagaaaaca tggttgcaa gggcttctcc 1920
393 ttctgggtct ggctggacaa tatcattgac cttgtgaaaa agtacatcct ggccctttgg 1980
395 aacgaagggt acatcatggg ctttatcagt aaggagcggg agcgggccat cttgagcact 2040
397 aagcctccag gcaccttctt gctaagattc agtgaaagca gcaaagaagg aggcgtcact 2100
399 ttcacttggg tggagaagga catcagcggg aagaccaga tccagtcctg ggaaccatac 2160
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409 accattgacc tgccgatgtc ccccccga cttagattcat tgatgcagtt tggaaataat 2460
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413 ttgacctcgg agtgcgctac ctcccccatg tgaggagctg agaacggaag ctgcagaaag 2580
415 atacgactga ggcgcctacc tgcattctgc caccctcac acagccaaac ccagatcat 2640
417 ctgaaactac taactttgtg gttccagatt ttttttaate tctacttct gctatctttg 2700
419 agcaatctgg gcacttttaa aaatagagaa atgagtgaat gtgggtgatc tgctttttatc 2760
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423 ctagagggag aaaaaggaaa tgtcttgtgt tgttttgttc ccctgccctc ctttctcagc 2880
425 agctttttgt tattgttgtt gttgttctta gacaagtgcc tcctggtgcc tgcggcatcc 2940
427 ttctgcctgt ttctgtaagc aaatgccaca ggccacctat agctacatac tcctggcatt 3000
429 gcacttttta accttgctga catccaaata gaagatagga ctatctaagc cctagggttc 3060
431 tttttaaat aagaaataat aacaattaaa gggcaaaaaa cactgtatca gcatagcctt 3120
433 tctgtattta agaaacttaa gcagccgggc atggtggctc acgctgtaa tcccagcact 3180
435 ttgggaggcc gaggcggatc ataaggtcag gagatgaaga ccatcctggc taacacgggtg 3240
437 aaaccccgtc tctactaaaa gtacaaaaaa ttagctgggt gtggtgggtg gcgcctgtag 3300
439 tcccagctac tcgggaggct gaggcaggag aatcgcttga acctgagagg cggaggttgc 3360
441 agtgagccaa aattgcacca ctgcacactg cactccatcc tgggcgacag tctgagactc 3420
443 tgtctcaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 3455

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446 &lt;210&gt; SEQ ID NO: 5

447 &lt;211&gt; LENGTH: 750

448 &lt;212&gt; TYPE: PRT

449 &lt;213&gt; ORGANISM: Homo sapiens

451 &lt;400&gt; SEQUENCE: 5

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454 1 5 10 15

457 Gln Val His Gln Leu Tyr Asp Asp Ser Phe Pro Met Glu Ile Arg Gln

RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : A:\A-71973.ST25.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; Xaa Pos. 1,2,3,4,5,7,8,9,11,12,13,14,15,16,17,18,19,20,21,22,24,25  
Seq#:8; Xaa Pos. 26,28,29,30,31,32  
Seq#:9; Xaa Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26  
Seq#:10; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23  
Seq#:10; Xaa Pos. 24,26,27,28,29  
Seq#:11; Xaa Pos. 7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26  
Seq#:12; Xaa Pos. 10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28  
Seq#:12; Xaa Pos. 29

**Invalid <213> Response:**

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:8,9,10,11,12

**VERIFICATION SUMMARY**

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Input Set : A:\A-71973.ST25.txt

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L:837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0  
M:341 Repeated in SeqNo=8  
L:862 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0  
M:341 Repeated in SeqNo=9  
L:901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0  
M:341 Repeated in SeqNo=10  
L:926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0  
M:341 Repeated in SeqNo=11  
L:955 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0  
M:341 Repeated in SeqNo=12